

This Raw Listing contains the General Information Section and up to the first 5 pages.

1 SEQUENCE LISTING

3 (1) General Information:

5 (i) APPLICANT: Gerard, Craig J.
6 Gerard, Norma P.
7 Mackay, Charles R.
8 Ponath, Paul D.
9 Post, Theodore W.
10 Qin, Shixin

ENTERED

12 (ii) TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
13 ANTAGONISTS THEREOF

15 (iii) NUMBER OF SEQUENCES: 18

17 (iv) CORRESPONDENCE ADDRESS:
18 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
19 (B) STREET: Two Militia Drive
20 (C) CITY: Lexington
21 (D) STATE: MA
22 (E) COUNTRY: USA
23 (F) ZIP: 02173

25
26 (v) COMPUTER READABLE FORM:

(V) COMPUTER READABLE FORM
27 (A) MEDIUM TYPE: Floppy disk
28 (B) COMPUTER: IBM PC compatible
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

32
33 (vi) CURRENT APPLICATION DATA:
34 (A) APPLICATION NUMBER:
35 (B) FILING DATE: 03-NOV-1997
36 (C) CLASSIFICATION:

37
38 (vii) PRIOR APPLICATION DATA:
39 (A) APPLICATION NUMBER: 08/720,565
40 (B) FILING DATE: 30-SEP-1996

41
42 (vii) PRIOR APPLICATION DATA:
43 (A) APPLICATION NUMBER: PCT/US96/00608
44 (B) FILING DATE: 19-JAN-1996

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46 (vii) PRIOR APPLICATION DATA:

46 (vii) PRIOR APPLICATION DATA:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/963,656DATE: 03/13/98
TIME: 16:53:55

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47 (A) APPLICATION NUMBER: US 08/375,199
48 (B) FILING DATE: 19-JAN-1995
49
50
51 (viii) ATTORNEY/AGENT INFORMATION:
52 (A) NAME: Brook, David E.
53 (B) REGISTRATION NUMBER: 22,592
54 (C) REFERENCE/DOCKET NUMBER: LKS94-05A2Z
55
56 (ix) TELECOMMUNICATION INFORMATION:
57 (A) TELEPHONE: 781-861-6240
58 (B) TELEFAX: 781-861-9540
59 (2) INFORMATION FOR SEQ ID NO:1:
60
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 1689 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: double
65 (D) TOPOLOGY: linear
66
67 (ii) MOLECULE TYPE: DNA (genomic)
68
69
70
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72
73 AATCCTTTTC CTGGCACCTC TGATATCCTT TTGAAATTCA TGTTAAAGAA TCCCTAGGCT 60
74 GCTATCACAT GTGGCATCTT TGTGAGTAC ATGAATAAAAT CAACTGGTGT GTTTACGAA 120
75 GGATGATTAT GCTTCATTGT GGGATTGTAT TTTTCTTCTT CTATCACAGG GAGAAGTGAA 180
76 ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG 240
77 GGCCTGCTCT GTGAAAAAGC TGATACCAGA GCACTGATGG CCCAGTTGTG GCCCCCCGCTG 300
78 TACTCCCTGG TGTTCACTGT GGGCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA 360
79 AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTCGGAC 420
80 CTGCTCTTCC TCGTCACCCCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGTT 480
81 TTTGGCCATG GCATGTGTAA GCTCCTCTCA GGGTTTTATC ACACAGGCTT GTACAGCGAG 540
82
83 ATCTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTT 600
84
85 GCCCTTCGAG CCCGGACTGT CACTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG 660
86 GCAGTGCTAG CAGCTCTTCC TGAATTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG 720
87 ACTCTTGCA GTGCTCTTCA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT 780
88 CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA 840

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100 GGAATCATCA AAACGCTGCT GAGGTGCCCT AGTAAAAAAA AGTACAAGGC CATCCGGCTC 900
101 ATTTTGTCATCA TCATGGCGGT GTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT 960
102 CTCTCTTCCT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGACGAA GCATCTGGAC 1020
103 CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCACT GCTGCATGAA CCCGGTGATC 1080
104 TACGCCCTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCAC TTG 1140
105 CTCATGCACC TGGGCAGATA CATCCCATT CTTCTAGTG AGAAGCTGGA AAGAACCGAC 1200
106 TCTGTCTCTC CATCCACAGC AGAGCCGGAA CTCTCTATTG TGTTTTAGGT AGATGCAGAA 1260
107 AATTGCCTAA AGAGGAAGGA CCAAGGAGAT NAAGCAAACA CATTAAGCCT TCCACACTCA 1320
108 CCTCTAAAAC AGTCCTTCAA ACCTTCCAGT GCAACACTGA AGCTCTTAAG AACTGAAAT 1380
109 ATACACACAG CAGTAGCAGT AGATGCATGT ACCCTAAGGT CATTACCACA GGCCAGGGCT 1440
110 GGGCAGCGTA CTCATCATCA ACCTAAAAAG CAGAGCTTG CTTCTCTCTC TAAAATGAGT 1500
111 TACCTATATT TTAATGCACC TGAATGTTAG ATAGTTACTA TATGCCGCTA CAAAAGGTA 1560
112 AAACTTTTA TATTTTATAC ATTAACATTCA GCCAGCTATT ATATAAATAA AACATTTCA 1620
113 CACAATACAA TAAGTTAATCT ATTATTTCTT CTAATGTGCC TAGTTCTTTC CCTGCTTAAT 1680
114 GAAAAGCTT 1689
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133 (2) INFORMATION FOR SEQ ID NO:2:
134
135 (i) SEQUENCE CHARACTERISTICS:
136 (A) LENGTH: 355 amino acids
137 (B) TYPE: amino acid
138 (C) STRANDEDNESS:
139 (D) TOPOLOGY: linear
140
141 (ii) MOLECULE TYPE: protein
142
143
144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
145
146 Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
147 1 5 10 15
148
149 Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
150 20 25 30
151
152 Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Phe Gly

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/963,656DATE: 03/13/98
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153 35 40 45
154
155 Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
156 50 55 60
157
158 Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
159 65 70 75 80
160
161 Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
162 85 90 95
163
164 His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
165 100 105 110
166
167 Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
168 115 120 125
169
170 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
171 130 135 140
172
173 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
174 145 150 155 160
175
176 Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
177 165 170 175
178
179 Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 180 185 190
181
182 Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
183 195 200 205
184
185 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
186 210 215 220
187
188 Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
189 225 230 235 240
190
191 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
192 245 250 255
193
194 Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
195 260 265 270
196
197 Cys Glu Arg Thr Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
198 275 280 285
199
200 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
201 290 295 300
202
203 Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
204 305 310 315 320
205

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206 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
207 325 330 335
208
209 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
210 340 345 350
211
212 Ile Val Phe
213 355
214
215
216

217 (2) INFORMATION FOR SEQ ID NO:3:

218
219 (i) SEQUENCE CHARACTERISTICS:
220 (A) LENGTH: 1193 base pairs
221 (B) TYPE: nucleic acid
222 (C) STRANDEDNESS: double
223 (D) TOPOLOGY: linear

224
225 (ii) MOLECULE TYPE: cDNA

226
227
228 (ix) FEATURE:
229 (A) NAME/KEY: CDS
230 (B) LOCATION: 92..1156

231
232
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

234
235 TTGTGCTTAT CCGGGCAAGA ACTTATCGAA ATACAATAGA AGACCCACGC GTCCGGTTTT 60
236
237 TACTTAGAAG AGATTTTCAG GGAGAAAGTGA A ATG ACA ACC TCA CTA GAT ACA 112
238 Met Thr Thr Ser Leu Asp Thr
239 1 5
240
241 GTT GAG ACC TTT GGT ACC ACA TCC TAC TAT GAT GAC GTG GGC CTG CTC 160
242 Val Glu Thr Phe Gly Thr Ser Tyr Tyr Asp Asp Val Gly Leu Leu
243 10 15 20
244
245 TGT GAA AAA GCT GAT ACC AGA GCA CTG ATG GCC CAG TTT GTG CCC CCG 208
246 Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe Val Pro Pro
247 25 30 35
248
249 CTG TAC TCC CTG GTG TTC ACT GTG GGC CTC TTG GGC AAT GTG GTG GTG 256
250 Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn Val Val Val
251 40 45 50 55
252
253
254
255 GTG ATG ATC CTC ATA AAA TAC AGG AGG CTC CGA ATT ATG ACC AAC ATC 304
256 Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met Thr Asn Ile
257 60 65 70
258

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/963,656**

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